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continued

RXA00657 (SEQ ID NO.:6) and in another case with the vector pB (SEQ ID NO.:125) carrying no additional insertion of nucleic acids.

In the Claims:

Please amend claims 1, 4, 25, 26, 27, 35, 38, 39, and 40 as follows:

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1. (Amended) An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein selected from the group consisting of a nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.

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4. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO: 5, or a complement thereof.

25. (Amended) The isolated polypeptide of claim 24, further comprising heterologous amino acid sequences.

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26. (Amended) An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO:5, or a complement thereof.

27. (Amended) An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 65% homologous to a nucleotide sequence set forth in SEQ ID NO:1, or a complement thereof.

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35. (Amended) The method of claim 28, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*.

Brevibacterium divaricatum, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.

38. (Amended) A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-6, alone or in combination with one or more metabolic pathway nucleic acid molecules.

39. (Amended) The method of claim 38, wherein the metabolic pathway nucleic acid molecule is selected from the group consisting of *metZ*, *metC*, *metB*, *metA*, *metE*, *metH*, *hom*, *asd*, *lysC*, *lysC /ask*, *rxa00657*, *dapA*, *dapB*, *dapC*, *dapD/argD*, *dapE*, *dapF*, *lysA*, *ddh*, *lysE*, *lysG*, *lysR*, *hsk*, *ppc*, *pycA*, *accD*, *accA*, *accB*, *accC*, *gpdh* genes encoding glucose-6-phosphate-dehydrogenase, *opcA*, *pgdh*, *ta*, *tk*, *pgl*, *rlpe*, *rpe* or any combination of the above-mentioned genes.

40. (Amended) The method of claim 38, wherein said metabolic pathway is methionine or lysine metabolism.

REMARKS

Claims 1, 4, 25, 26, 27, 35, 38, 39, and 40 have been amended. Support for the amendments to the claims may be found in the original claims as filed and in the specification. Specifically, claims 25, 35, 39, and 40 have been amended to correct dependency of the claims. Claims 1, 4, and 38 have been amended to correct typographical errors in the claims. The specification has also been amended to correct typographical errors and to correct sequence listing identifiers.

In accordance with 37 C.F.R. § 1.825, Applicants submit herewith substitute pages 1-176 which contain substitute Sequence Listing for the above-referenced application. The specification has been amended to include substitute pages 1-176.